

## GENE BANKS FOR THE PRESERVATION OF WILD APPLE GENETIC RESOURCES

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(Received August 12, 2004/Accepted March 10, 2005)

### A B S T R A C T

The center of genetic diversity for the genus *Malus* lies in east Asia. The diversity of wild and cultivated apples constitutes an enormous and irretrievable gene pool, and needs to be preserved for future generations in gene banks. These gene banks can be either decentralized or centralized. Decentralized gene banks include the places where different genotypes are discovered, such as in the wild or on farms. In centralized gene banks, the genotypes may be propagated either by grafting or by seed. Centralized collections of wild and cultivated apple genotypes have existed for decades. In most cases, the original material had been collected a long time ago, and has been exchanged among various arboreta, often as self-pollinated seed. Passport data on these genotypes are often incomplete.

In order to most efficiently exploit the genetic potential contained in gene banks, it is necessary to thoroughly and systematically evaluate the genotypes in terms of the desirable traits that they may donate in future breeding programs. The main emphasis has been on identifying potential donors of resistance to biotic and abiotic stressors.

Over the last fifteen years, there has been a lot of interest in collecting wild *Malus* species from the areas in which the apple had originally been domesticated. This is important for understanding how, when and where the apple had been domesticated. Screening of seedlings from different regions indicates that some of them are potential

donors of valuable resistance genes. Furthermore, these new genotypes will fill out current collections of wild apple genotypes. Most current collections contain a very limited number of accessions for each *Malus* species. This does not adequately reflect the diversity and potential of each species. Molecular marker methods are now being used to more efficiently evaluate new accessions in new and existing core collections.

Research on wild *Malus* species can be shared by different working groups all over the world. International cooperation can increase our knowledge about the genus and enlarge the genetic base available for future apple breeding programs.

**Key words:** *Malus sieversii*, *Malus domestica*, genetic center, domestication of apple, gene bank, *ex situ* conservation

## INTRODUCTION

The center of genetic diversity for the genus *Malus* lies in east Asia. In the mountains of western and southwestern China, up to twenty different wild species can be found (Zhou, 1999). To the west, from central Asia to central Europe, several species with relatively large fruit evolved. Chief among them is *M. sieversii* (Fig. 1), the species which probably contributes most to the genetic makeup of the cultivated apple (*Malus x domestica*).



**Figure 1.** *Malus sieversii*, the main source of genetic material in the cultivated apple, growing at the Fruit Gene Bank in Dresden-Pillnitz, Germany (photo: M. Fischer)



**Figure 2.** *Malus orientalis*, a minor source of genetic material in cultivated apple cultivars from the Caucasus (photo: M. Fischer)

Apple cultivation move westward very early in history. Apples were cultivated in Asia Minor and the Levant as early as 6500 BC. Later, apple cultivation spread north along the various branches of the silk road. Along the way, genetic material from *M. orientalis* (Fig. 2) and *M. sylvestris* var. *praecox* from the Caucasus and south-eastern Russia found their way into the apple gene pool. It is possible that apple cultivation also spread through central Russia. However, *M. sylvestris* var. *sylvestris*, indigenous to central Europe, did not play a role in the domestication of the apple. Apple cultivation came to Greece before the ninth century BC, and was later spread by the Romans throughout the Mediterranean and central Europe (Ponomarenko, 1987).

Meanwhile, in the orient, a second domesticated apple species arose, *M. x asiatica* (Fig. 3). It is believed to be the product of a crossing of *M. sieversii* from western China and *M. baccata* from east Asia, and has been grown locally for centuries (Ponomarenko, 1991).



**Figure 3.** *Malus x asiatica*, a local cultivar, growing at the Fruit Gene Bank in Dresden-Pillnitz, Germany (photo: M. Fischer)

The genus *Malus* consists of about thirty wild species and thousands of domesticated cultivars. The diversity of wild and cultivated apples constitutes an enormous and irretrievable gene pool, and needs to be preserved for future generations in gene banks.

## PRESERVATION

*Malus* gene banks can be either decentralized or centralized.

Decentralized gene banks include places where different wild or domesticated genotypes are discovered, such as in the wild or on farms. For



**Figure 4.** Stand of *Malus sieversii* growing at 1300 meters above sea level in Kazakhstan (photo: P.L. Forsline)

example, in the northern Caucasus, central Asia, and Kazakhstan (Fig. 4), wild species can be found in natural forests and nature reserves. Specimens of old, local cultivars, on the other hand, are often encountered on farms. These old cultivars often have been bred to suit local conditions.

In centralized gene banks, wild species may be either propagated as seedlings or preserved in seed banks. Propagation by seedlings is usually performed more for evaluation than for actual preservation of genetic material. Both wild species and domesticated cultivars are also propagated by grafting. Seeds of wild species can be kept viable for over fifty years at minus 20°C. Dormant scions have also been cryo-preserved in liquid nitrogen for eight years with no loss of viability (Forsline et al., 1998).

## CENTRALIZED COLLECTIONS

Centralized collections of wild and cultivated apple genotypes have existed for decades. In most cases, the original material had been collected a long time ago, and has been exchanged among various arboreta, often as self-pollinated seed. Passport data on these genotypes are often incomplete.

Centralized collections with a long-standing reputation for superb scientific research are found in several countries. In Russia, the main collection is located at the VIR in Saint Peterburg, which also has various branch collections throughout Russia and the countries which once were part of the Soviet Union. Scientists who have worked at the VIR include Vavilov, Vasil'cenko and Ponomarenko. In the United States, the most important collections are in Geneva, New York and at the Arnold Arboretum in Massachusetts. Scientists who have worked in Geneva include Way, Lamb and Forsline. Scientists who have worked at the Arnold Arboretum include Hansen and Rehder. In the United Kingdom, the most important collections are at the Royal Botanic Gardens at Kew and at Wye College. Scientists who have worked at Kew include Hillier. Scientists who have worked at Wye College include Watkins and Lamcont. In Germany, the most important collection was at Naumburg, and has been moved to Dresden-Pillnitz. Scientists who have worked at Naumburg or Dresden-Pillnitz include Sax, Mildenerger, Büttner and Geibel.

## RECENT COLLECTION EXPEDITIONS

Over the last fifteen years, there has been a lot of interest in collecting wild *Malus* species from the areas in which the apple had originally been domesticated (Forsline, 1996; Hokanson et al., 1997; Forsline, 2000; Luby et al., 2000; Geibel et al., 2004). Different gene banks have been filling out their collections with seeds collected from different regions, especially Asia. This is important for understanding how, when and where the apple had been domesticated. Screening of seedlings from different regions indicates that some of them are potential donors of valuable resistance genes.

Current expeditions are underway to collect various wild species, including *M. sieversii* from Kazakhstan, *M. orientalis* from Russia and Turkey, *M. baccata* from Russia and China, *M. coronaria*, *M. ioensis*, *M. fusca* from the United States, *M. sylvestris* from Germany, and other *Malus* species from China.

## EVALUATION

The various species collected are being evaluated under natural or artificial conditions according to numerous objective and subjective methods. All interesting traits are carefully documented. The main emphasis has been on identifying potential donors of resistance to biotic and abiotic stressors and determining the genetic mechanisms at work.

Ways to reintroduce wild *Malus* species into natural forests are also being developed. Work is also underway to preserve stands of wild species on nature reserves in the United States, Kazakhstan and the Caucasus.

Because of the extent of their natural range, research on wild *Malus* species is being carried out on an international basis. All results are carefully documented and stored in international electronic databases so that they can be freely interchanged among interested institutions.

## CONCLUDING REMARKS

Further expeditions to collect wild *Malus* species are needed because the original habitats of most accessions in current collections are unknown. Also, most current collections contain only a few accessions of many wild species. This does not adequately reflect the diversity and potential of each species. Further expeditions should concentrate on China, which has the highest diversity of wild *Malus* species.

Molecular marker methods are now being used to more efficiently evaluate new accessions in new and existing core collections (Forsline, 1996; Hokanson et al., 1998; Fischer et al., 2003; Fischer et al., 2004). There is a lot of work to be done on documenting and processing the evaluation results for storage in electronic databases.

Research on wild *Malus* species can be shared by different working groups all over the world. International cooperation can increase our knowledge about the genus and enlarge the genetic base available for future apple breeding programs.

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## OCHRONA ZASOBÓW GENOWYCH DZIKICH JABŁONI

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### S T R E S Z C Z E N I E

Największa liczba dziko rosnących gatunków z rodzaju *Malus* jest spotykana w Azji Wschodniej. Różne dziko rosnące i uprawiane jabłonie stanowią ogromną i nieodwracalną pulę genów, która powinna zostać zachowana dla przyszłych pokoleń w formie banku genów. Bank genów może być zarówno w formie scentralizowanej, jak i zdecentralizowanej. Forma zdecentralizowana banku genów obejmuje miejsca, gdzie różne genotypy jabłoni zostały odkryte w stanowiskach naturalnych lub w gospodarstwach. W formie scentralizowanej bank genów zakłada się rozmnażając poszczególne genotypy przez nasiona lub szczepienie. Scentralizowane kolekcje dziko rosnących i uprawianych odmian jabłoni mają istnieć przez dziesięciolecia. W większości przypadków oryginalny materiał roślinny został zgromadzony dawno temu i jest przedmiotem wymiany pomiędzy zainteresowanymi nim placówkami naukowymi, także w formie nasion. Dane paszportowe tych genotypów są często niekompletne.

W celu lepszego wykorzystania potencjału genetycznego zgromadzonego w bankach genów należy prowadzić systematyczną i szczegółową ocenę poszczególnych genotypów pod względem cech, które mogą mieć duże znaczenie w tworzeniu przyszłych programów hodowlanych. Główny nacisk powinien być położony na identyfikację genów, które mogą być źródłem odporności na biotyczne i abiotyczne stresy.

Przez ostatnich piętnaście lat obserwuje się duże zainteresowanie gromadzeniem dziko rosnących gatunków z rodzaju *Malus* z obszarów, gdzie jabłoń stała się po raz pierwszy przedmiotem uprawy przez człowieka. Jest to ważne dla zrozumienia, kiedy i gdzie jabłoń została udomowiona. Badania siewek wyprodukowanych z nasion pochodzących z różnych regionów wskazują, że są wśród nich okazy posiadające wartościowe geny odporności. Te nowe genotypy wypełniają także obecne kolekcje dzikich jabłoni. Większość kolekcji zawiera ograniczoną liczbę poszczególnych gatunków z rodzaju *Malus*. Dlatego nie odzwierciedla to w pełni różnorodności każdego z nich. Obecnie za pomocą markerów molekularnych prowadzi się bardziej szczegółowe badania nowo pozyskanych taksonów w kolekcjach.

Badania dotyczące dzikich gatunków z rodzaju *Malus* są prowadzone przez różne zespoły na całym świecie. Współpraca międzynarodowa w tym zakresie może przyczynić się do podniesienia poziomu naszej wiedzy na temat genów i powiększyć bazę genetyczną dostępną dla hodowców nowych odmian jabłoni w przyszłości.

**Słowa kluczowe:** *Malus sieversii*, *Malus domestica*, centrym genetyczne, udomowienie jabłoni, bank genów, *ex situ* ochrona